SEQUENCE LISTING

<110> Schlievert, Patrick M.
Roggiani, Manuela
Stoehr, Jennifer
Ohlendorf, Douglas

<120> MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE

<130> 600.311USWO

<140> US 08/973,391
<141> 1998-03-12

<150> PCT/US96/10252
<151> 1996-06-07

<150> US 08/480,261
<151> 1995-06-07

<160> 14

<170> PatentIn version 3.1

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ttttgttatt ttataataaa attattaata taagttaatg ttttttaaaa atatacaatt 720

ttattctatt tatagttagc tatttttttca ttgttagtaa tattggtgaa ttgtaataac 780

cttttttaaat ctagaggaga acccagatat aaaatggagg aatatta atg gaa aac 836
Met Glu Asn
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aat aaa aaa gta ttg aag aaa atg gta ttt ttt gtt tta gtg aca ttt 884
Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu Val Thr Phe
5 10 15

ctt gga cta aca atc tcg caa gag gta ttt gct caa caa gac ccc gat 932
Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln Asp Pro Asp
20 25 30 35

cca agc caa ctt cac aga tct agt tta gtt aaa aac ctt caa aat ata 980
Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile
40 45 50

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tat ttt ctt tat gag ggt gac cct gtt act cac gag aat gtg aaa tct      1028
Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser
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gtt gat caa ctt tta tct cac cat tta ata tat aat gtt tca ggg cca      1076
Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro
        70                  75                  80

aat tat gat aaa tta aaa act gaa ctt aag aac caa gag atg gca act      1124
Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr
    85                  90                  95

tta ttt aag gat aaa aac gtt gat att tat ggt gta gaa tat tac cat      1172
Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His
100                 105                 110                 115

ctc tgt tat tta tgt gaa aat gca gaa agg agt gca tgt atc tac gga      1220
Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly
                120                 125                 130

ggg gta aca aat cat gaa ggg aat cat tta gaa att cct aaa aag ata      1268
Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile
            135                 140                 145

gtc gtt aaa gta tca atc gat ggt atc caa agc cta tca ttt gat att      1316
Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile
        150                 155                 160

gaa aca aat aaa aaa atg gta act gct caa gaa tta gac tat aaa gtt      1364
Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val
    165                 170                 175

aga aaa tat ctt aca gat aat aag caa cta tat act aat gga cct tct      1412
Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser
180                 185                 190                 195

aaa tat gaa act gga tat ata aag ttc ata cct aag aat aaa gaa agt      1460
Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu Ser
                200                 205                 210

ttt tgg ttt gat ttt ttc cct gaa cca gaa ttt act caa tct aaa tat      1508
Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr
            215                 220                 225

ctt atg ata tat aaa gat aat gaa acg ctt gac tca aac aca agc caa      1556
Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln
        230                 235                 240

att gaa gtc tac cta aca acc aag taa ctttttgctt ttggcaacct            1603
Ile Glu Val Tyr Leu Thr Thr Lys
    245                 250

tacctactgc tggatttaga aattttattg caattctttt attaatgtaa aaaccgctca    1663

tttgatgagc ggttttgtct tatctaaagg agctttacct cctaatgctg caaaatttta    1723

aatgttggat ttttgtattt gtctattgta tttgatgggt aatcccattt ttcgacagac    1783

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ttatcgtc 1851

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Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu
35 40 45

Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn
50 55 60

Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val
65 70 75 80

Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu
85 90 95

Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu
100 105 110

Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys
115 120 125

Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro
130 135 140

Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser
145 150 155 160

Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp
165 170 175

Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn
180 185 190

Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn
195 200 205

Lys Glu Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln
210 215 220

Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn
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Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys
245 250

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Glu Asn Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr
35 40 45

Asn Val Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn
50 55 60

Gln Glu Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly
65 70 75 80

Val Glu Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser
85 90 95

Ala Cys Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu
100 105 110

Ile Pro Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser
115 120 125

Leu Ser Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu
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Leu Asp Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr
145 150 155 160

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Thr Asn Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro
                165                 170                 175

Lys Asn Lys Glu Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe
            180                 185                 190

Thr Gln Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp
        195                 200                 205

Ser Asn Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys
    210                 215                 220
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